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b) generating recombinant libraries comprising said RRT-SH3 domains, and

c) subjecting said libraries to affinity or functional selection steps to identify artificial SH3 domains.

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17. (amended) The method according to claim 3, wherein the six amino acids that are replaced in the RT-loop are replaced with a peptide motif derived from Hck-SH3 and targeted to the HIV-1 Nef protein selected from the group consisting of XSWSXX (SEQ ID NO:28), XSPFXX (SEQ ID NO:30) and XSXFPW (SEQ ID NO:32), wherein X is any amino acid.
